

## RAW SEQUENCE LISTING

DATE: 01/03/2002

PATENT APPLICATION: US/09/900,590A

TIME: 11:31:32

Input Set : N:\Crf3\RULE60\09900590A.raw

Output Set: N:\CRF3\01032002\I900590A.raw

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APR 0 1 2002

TECH CENTER 1600/2900

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Huse, William D.

6 Glaser, Scott M.

8 (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

9 Antibodies, Nucleic Acids Encoding Same and Methods of

Use

11 (iii) NUMBER OF SEQUENCES: 100

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Campbell &amp; Flores LLP

15 (B) STREET: 4370 La Jolla Village Drive, Suite 700

16 (C) CITY: San Diego

17 (D) STATE: California

18 (E) COUNTRY: United States

19 (F) ZIP: 92122

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

C--&gt; 28 (A) APPLICATION NUMBER: US/09/900,590A

C--&gt; 29 (B) FILING DATE: 06-Jul-2001

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/016,061

34 (B) FILING DATE:

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Campbell, Cathryn A.

38 (B) REGISTRATION NUMBER: 31,815

39 (C) REFERENCE/DOCKET NUMBER: P-IX 2965

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: (619) 535-9001

43 (B) TELEFAX: (619) 535-8949

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 351 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: both

52 (D) TOPOLOGY: linear

55 (ix) FEATURE:

56 (A) NAME/KEY: CDS

57 (B) LOCATION: 1..351

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62 CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG

63 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

64 1 5 10 15

66 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT

48

96

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67 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
68          20          25          30
70 GAC ATG TCT TGG GTT CGC CAG GCT CCG GGC AAG GGT CTG GAG TGG GTC      144
71 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
72          35          40          45
74 GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG      192
75 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
76          50          55          60
78 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT AGT AAG AAC ACC CTA TAC      240
79 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
80 65          70          75          80
82 CTG CAA ATG AAC TCT CTG AGA GCC GAG GAC ACA GCC GTG TAT TAC TGT      288
83 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
84          85          90          95
86 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT ACA      336
87 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
88          100          105          110
90 GTG ACT GTT TCT AGT      351
91 Val Thr Val Ser Ser
92          115

```

## 95 (2) INFORMATION FOR SEQ ID NO: 2:

## 97 (i) SEQUENCE CHARACTERISTICS:

98 (A) LENGTH: 117 amino acids

99 (B) TYPE: amino acid

100 (D) TOPOLOGY: linear

102 (ii) MOLECULE TYPE: protein

104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

106 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
107 1          5          10          15
109 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
110          20          25          30
112 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
113          35          40          45
115 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
116          50          55          60
118 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
119 65          70          75          80
121 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
122          85          90          95
124 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
125          100          105          110
127 Val Thr Val Ser Ser
128          115

```

## 130 (2) INFORMATION FOR SEQ ID NO: 3:

## 132 (i) SEQUENCE CHARACTERISTICS:

133 (A) LENGTH: 321 base pairs

134 (B) TYPE: nucleic acid

135 (C) STRANDEDNESS: both

136 (D) TOPOLOGY: linear

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139      (ix) FEATURE:
140          (A) NAME/KEY: CDS
141          (B) LOCATION: 1..321
142
143      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
144      GAG ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT CTC AGC CCA GGA      48
145      Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
146      1      5      10      15
147      GAA AGG GCG ACT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC      96
148      Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
149      20      25      30
150      CTA CAC TGG TAT CAA CAA AGG CCT GGT CAA GCC CCA AGG CTT CTC ATC      144
151      Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
152      35      40      45
153      AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC GCC AGG TTC AGT GGC      192
154      Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
155      50      55      60
156      AGT GGA TCA GGG ACA GAT TTC ACC CTC ACT ATC TCC AGT CTG GAG CCT      240
157      Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
158      65      70      75      80
159      GAA GAT TTT GCA GTC TAT TAC TGT CAA CAG AGT GGC AGC TGG CCT CAC      288
160      Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
161      85      90      95
162      ACG TTC GGA GGG GGG ACC AAG GTG GAA ATT AAG      321
163      Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
164      100      105
165
166      (2) INFORMATION FOR SEQ ID NO: 4:
167          (i) SEQUENCE CHARACTERISTICS:
168              (A) LENGTH: 107 amino acids
169              (B) TYPE: amino acid
170              (D) TOPOLOGY: linear
171
172          (ii) MOLECULE TYPE: protein
173
174          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
175      Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
176      1      5      10      15
177      Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
178      20      25      30
179      Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
180      35      40      45
181      Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
182      50      55      60
183      Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
184      65      70      75      80
185      Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
186      85      90      95
187      Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
188      100      105
189
190      (2) INFORMATION FOR SEQ ID NO: 5:
191          (i) SEQUENCE CHARACTERISTICS:
192              (A) LENGTH: 351 base pairs

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211         (B) TYPE: nucleic acid
212         (C) STRANDEDNESS: both
213         (D) TOPOLOGY: linear
216     (ix) FEATURE:
217         (A) NAME/KEY: CDS
218         (B) LOCATION: 1..351
221     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
223 GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA AGG      48
224 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
225   1           5           10           15
227 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT AGC TAT      96
228 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
229           20           25           30
231 GAC ATG TCT TGG GTT CGC CAG ATT CCG GAG AAG AGG CTG GAG TGG GTC      144
232 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
233           35           40           45
235 GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG      192
236 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
237           50           55           60
239 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTA TAC      240
240 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
241           65           70           75           80
243 CTG CAA ATG AGC AGT CTG AAC TCT GAG GAC ACA GCC ATG TAT TAC TGT      288
244 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
245           85           90           95
247 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT CTG      336
248 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
249           100          105          110
251 GTC ACT GTC TCT GCA      351
252 Val Thr Val Ser Ala
253           115
256 (2) INFORMATION FOR SEQ ID NO: 6:
258     (i) SEQUENCE CHARACTERISTICS:
259         (A) LENGTH: 117 amino acids
260         (B) TYPE: amino acid
261         (D) TOPOLOGY: linear
263     (ii) MOLECULE TYPE: protein
265     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
267 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
268   1           5           10           15
270 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
271           20           25           30
273 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
274           35           40           45
276 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
277           50           55           60
279 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
280           65           70           75           80
282 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys

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283          85          90          95
285 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
286          100          105          110
288 Val Thr Val Ser Ala
289          115
291 (2) INFORMATION FOR SEQ ID NO: 7:
293   (i) SEQUENCE CHARACTERISTICS:
294       (A) LENGTH: 321 base pairs
295       (B) TYPE: nucleic acid
296       (C) STRANDEDNESS: both
297       (D) TOPOLOGY: linear
300   (ix) FEATURE:
301       (A) NAME/KEY: CDS
302       (B) LOCATION: 1..321
305   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
307 GAT ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT GTG ACA CCA GGA      48
308 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
309  1          5          10          15
311 GAT AGC GTC AGT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC      96
312 Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
313          20          25          30
315 CTA CAC TGG TAT CAA CAA AAA TCA CAT GAG TCT CCA AGG CTT CTC ATC      144
316 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
317          35          40          45
319 AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC TCC AGG TTC AGT GGC      192
320 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
321          50          55          60
323 AGT GGA TCA GGG ACA GAT TTC GCT CTC AGT ATC AAC AGT GTG GAG ACT      240
324 Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
325  65          70          75          80
327 GAA GAT TTT GGA ATG TAT TTC TGT CAA CAG AGT GGC AGC TGG CCT CAC      288
328 Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
329          85          90          95
331 ACG TTC GGA GGG GGG ACC AAG CTG GAA ATT AAG      321
332 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
333          100          105
336 (2) INFORMATION FOR SEQ ID NO: 8:
338   (i) SEQUENCE CHARACTERISTICS:
339       (A) LENGTH: 107 amino acids
340       (B) TYPE: amino acid
341       (D) TOPOLOGY: linear
343   (ii) MOLECULE TYPE: protein
345   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
347 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
348  1          5          10          15
350 Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
351          20          25          30
353 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
354          35          40          45

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VERIFICATION SUMMARY

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TIME: 11:31:33

Input Set : N:\Crf3\RULE60\09900590A.raw

Output Set: N:\CRF3\01032002\I900590A.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31

L:773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32